

05/30
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See page 6



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RAW SEQUENCE LISTING

DATE: 05/30/2002

PATENT APPLICATION: US/10/029,345A

TIME: 10:20:21

Input Set : A:\D0072.NP.msg.parts.ST25.txt

Output Set: N:\CRF3\05302002\J029345A.raw

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3 <110> APPLICANT: Bristol-Myers Squibb Company
5 <120> TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES
7 <130> FILE REFERENCE: D0072.NP
9 <140> CURRENT APPLICATION NUMBER: US 10/029,345A
10 <141> CURRENT FILING DATE: 2001-12-20
12 <150> PRIOR APPLICATION NUMBER: US 60/256,868
13 <151> PRIOR FILING DATE: 2000-12-20
15 <150> PRIOR APPLICATION NUMBER: US 60/280,186
16 <151> PRIOR FILING DATE: 2001-03-30
18 <150> PRIOR APPLICATION NUMBER: US 60/287,735
19 <151> PRIOR FILING DATE: 2001-05-01
21 <150> PRIOR APPLICATION NUMBER: US 60/295,848
22 <151> PRIOR FILING DATE: 2001-06-05
24 <150> PRIOR APPLICATION NUMBER: US 60/300,465
25 <151> PRIOR FILING DATE: 2001-06-25
27 <160> NUMBER OF SEQ ID NOS: 208
29 <170> SOFTWARE: PatentIn version 3.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 144
33 <212> TYPE: DNA
34 <213> ORGANISM: HOMO SAPIENS
36 <400> SEQUENCE: 1
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41 catgcagggc ttggtcgaac aggt                                           144
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 48
46 <212> TYPE: PRT
47 <213> ORGANISM: HOMO SAPIENS
49 <400> SEQUENCE: 2
51 Leu Val Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser
52 1              5              10              15
54 Leu Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe Ala Leu Gln
55              20              25              30
57 Glu Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly Arg Thr Gly
58              35              40              45
60 <210> SEQ ID NO: 3
61 <211> LENGTH: 33
62 <212> TYPE: DNA
63 <213> ORGANISM: HOMO SAPIENS
65 <400> SEQUENCE: 3
66 gatgtcttct gggccctcct gtggaacaca gtt                                           33
69 <210> SEQ ID NO: 4

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70 <211> LENGTH: 11
71 <212> TYPE: PRT
72 <213> ORGANISM: HOMO SAPIENS
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77 1 5 10
79 <210> SEQ ID NO: 5
80 <211> LENGTH: 746
81 <212> TYPE: DNA
82 <213> ORGANISM: HOMO SAPIENS
84 <400> SEQUENCE: 5
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87 ctgggtgctt ccgggcgcgcg tggcgggact ggcgctgccc cggctccccg cccactacca 120
89 gttctgtgtg gacctgggcg tgcggcacct ggtgtccctg acggagcgcg ggccccctca 180
91 cagcgacagc tgcgcgcgcg tcacctgca ccgctgcgc atccccgact tctgccgcgc 240
93 ggcccccgac cagatcgacc gcttcgtgca gatcgtggac gagggcaacg cacggggaga 300
95 ggctgtggga gtgcactgtg ctctgggctt tggcgcact ggcaccatgc tggcctqta 360
97 cctggtgaag gagcggggct tggctgcagg agatgccatt gctgaaatcc gacgactacg 420
99 acccggcccc atcgagacct atgagcagga gaaagcagtc ttccagttct accagcgaac 480
101 gaaataaggg gccttagtac ccttctacca ggccctcact ccccttcccc atgttgtcga 540
103 tggggccaga gatgaaggga agtggaactaa agtattaaac cctctagctc ccattggctg 600
105 aagacactga agtagccac cctgcaggc aggtcctgat tgaaggggag gcttgtaactg 660
107 ctttgttgaa taaatgagtt ttacgaacca gggaaaaaaaa aaaaaaaaaa aaagaaaaaa 720
109 aaaaaaaaaa aaaaaaaaaa aaagaa 746
112 <210> SEQ ID NO: 6
113 <211> LENGTH: 248
114 <212> TYPE: PRT
115 <213> ORGANISM: HOMO SAPIENS
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118 <221> NAME/KEY: VARIANT
119 <222> LOCATION: (162)..(162)
120 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
123 <220> FEATURE:
124 <221> NAME/KEY: VARIANT
125 <222> LOCATION: (200)..(200)
126 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
129 <220> FEATURE:
130 <221> NAME/KEY: VARIANT
131 <222> LOCATION: (203)..(203)
132 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
135 <220> FEATURE:
136 <221> NAME/KEY: VARIANT
137 <222> LOCATION: (214)..(214)
138 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
141 <220> FEATURE:
142 <221> NAME/KEY: VARIANT
143 <222> LOCATION: (224)..(224)
144 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
147 <400> SEQUENCE: 6

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149 Trp Pro Gly Arg Arg Arg Gly Gln Val Gly Ala Met Gly Val Gln Pro
150 1 5 10 15
152 Pro Asn Phe Ser Trp Val Leu Pro Gly Arg Leu Ala Gly Leu Ala Leu
153 20 25 30
155 Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu Asp Leu Gly Val Arg
156 35 40 45
158 His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro His Ser Asp Ser Cys
159 50 55 60
161 Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro Asp Phe Cys Pro Pro
162 65 70 75 80
164 Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile Val Asp Glu Ala Asn
165 85 90 95
167 Ala Arg Gly Glu Ala Val Gly Val His Cys Ala Leu Gly Phe Gly Arg
168 100 105 110
170 Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys Glu Arg Gly Leu Ala
171 115 120 125
173 Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu Arg Pro Gly Pro Ile
174 130 135 140
176 Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln Phe Tyr Gln Arg Thr
177 145 150 155 160
W--> 179 Lys Xaa Gly Ala Leu Val Pro Phe Tyr Gln Ala Leu Thr Pro Leu Pro
180 165 170 175
182 His Val Val Asp Gly Ala Arg Asp Glu Gly Lys Trp Thr Lys Val Leu
183 180 185 190
W--> 185 Asn Pro Leu Ala Pro Ile Gly Xaa Arg His Xaa Ser Ser Pro Pro Leu
186 195 200 205
W--> 188 Gln Ala Gly Pro Asp Xaa Arg Gly Gly Leu Tyr Cys Phe Val Glu Xaa
189 210 215 220
191 Met Ser Phe Thr Asn Gln Gly Lys Lys Lys Lys Lys Lys Arg Lys Lys
192 225 230 235 240
194 Lys Lys Lys Lys Lys Lys Lys Arg
195 245
197 <210> SEQ ID NO: 7
198 <211> LENGTH: 511
199 <212> TYPE: DNA
200 <213> ORGANISM: HOMO SAPIENS
202 <400> SEQUENCE: 7
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205 attacacaca acccaaccaa tacctacttt aatagattct tacaggaact taagcaggat 120
207 qaggttacca ccatagtaag agtatgaaaa gcaacttaca acattgctct tttagagaag 180
209 ggaagcatcc aggttccgga ctggcctttt gatgatggta cagcaccatc cagccagata 240
211 attgataact ggtaaaaact tatgaaaaat aaatttcatt aagatcctgg ttgttgtatt 300
213 gcaattcact gtgttgtagg ttttgggtga gctccagttg ctagttgccc tagctttaat 360
215 tgaagggtga atgaaatatg aaaatgtagt acagttcatc agataaaaagt gacatggaac 420
217 ttttaacagc aaacaacttt tgtatttgga gaaatattgt cttaaaatat gcttgcacct 480
219 cagaaatccc agaaataact gtttccttca g 511
222 <210> SEQ ID NO: 8
223 <211> LENGTH: 170
224 <212> TYPE: PRT

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225 <213> ORGANISM: HOMO SAPIENS
227 <220> FEATURE:
228 <221> NAME/KEY: Variant
229 <222> LOCATION: (49)..(49)
230 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
233 <220> FEATURE:
234 <221> NAME/KEY: Variant
235 <222> LOCATION: (166)..(166)
236 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
239 <220> FEATURE:
240 <221> NAME/KEY: Variant
241 <222> LOCATION: (142)..(142)
242 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
245 <220> FEATURE:
246 <221> NAME/KEY: Variant
247 <222> LOCATION: (110)..(110)
248 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
251 <220> FEATURE:
252 <221> NAME/KEY: Variant
253 <222> LOCATION: (121)..(121)
254 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
257 <220> FEATURE:
258 <221> NAME/KEY: Variant
259 <222> LOCATION: (127)..(127)
260 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
263 <220> FEATURE:
264 <221> NAME/KEY: Variant
265 <222> LOCATION: (155)..(155)
266 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
269 <400> SEQUENCE: 8
271 Met Ala Arg Met Asn Leu Pro Ala Ser Val Asp Ile Ala Tyr Lys Asn
272 1 5 10 15
274 Val Arg Phe Leu Ile Thr His Asn Pro Thr Asn Thr Tyr Phe Asn Arg
275 20 25 30
277 Phe Leu Gln Glu Leu Lys Gln Asp Gly Val Thr Thr Ile Val Arg Val
278 35 40 45
W--> 280 Xaa Lys Ala Thr Tyr Asn Ile Ala Leu Leu Glu Lys Gly Ser Ile Gln
281 50 55 60
283 Val Pro Asp Trp Pro Phe Asp Asp Gly Thr Ala Pro Ser Ser Gln Ile
284 65 70 75 80
286 Ile Asp Asn Trp Leu Lys Leu Met Lys Asn Lys Phe His Glu Asp Pro
287 85 90 95
W--> 289 Gly Cys Cys Ile Ala Ile His Cys Val Val Gly Phe Gly Xaa Ala Pro
290 100 105 110
W--> 292 Val Ala Ser Cys Pro Ser Phe Asn Xaa Arg Trp Asn Glu Ile Xaa Lys
293 115 120 125
W--> 295 Cys Ser Thr Val His Gln Ile Lys Val Thr Trp Asn Phe Xaa Gln Gln
296 130 135 140
W--> 298 Thr Thr Phe Val Phe Gly Glu Ile Leu Ser Xaa Asn Met Leu Ala Pro

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299 145          150          155          160
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302          165          170
304 <210> SEQ ID NO: 9
305 <211> LENGTH: 1710
306 <212> TYPE: DNA
307 <213> ORGANISM: HOMO SAPIENS
309 <400> SEQUENCE: 9
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312 gaggagctga aggaggtgag caaggagcag cccagactgg aggcctgagta ccttgccaac      120
314 accaccaaga actgttaacc acatgtgcta cccatgacc actccagggt caggctgacc      180
316 cagctggagg gagagcctca ttctgactac atcaatgcc aacttggtccc aggcctacacc      240
318 cgcgccacag agttcattgc ctctcagggg cctctcaaga aaacactgga gaacttctgg      300
320 cggctggtgc gggagcagca ggtccgcata atcatcatgc cgaccatcag catggagaac      360
322 gggaggtgac tgtgtgagca ttactggctg accgactcta ccccggaac ccattggtcac      420
324 atcaccatcc acctcctagc tgaggagcct gaggatgagt ggaccaagcg ggaattccag      480
326 ctgcagcagc ttgtccagca acatcaacgg aggggtggagc aactgcagtt caccacctga      540
328 tccgaccaca gcataccttga ggctcccagc tccctgctcg cctttatgga gctggtacag      600
330 tagcaggcaa gggccaccca gggcgtggga cccatcctgg tgcactgcag gggctgtccc      660
332 tgcgtgtgtg gcattggcgc gacaggcacc ttctgtggcc tgtcagaggt gctgcagcag      720
334 ctggaggagg agcagatggt agacgtgttc catgctgtgt atgcactccg gatgcaccag      780
336 cccctcatga tccagacctt gaggcagtac gtcttctctg acagctgctt actgaacaag      840
338 attctggaag gaccttcaa catctctgag tcttgccca tctctgtgac ggacctccc      900
340 caggcgtgtg ccaagagggc agccagtgcc aatgctggct tcttgaagga gtacgaggcc      960
342 atcaaggacg aggcctggtt ttccgcacc ccgcctggct atgagcagga cagccccgtc     1020
344 tccatgaccg gttctcaagg gcagttttct ccggtggagg agagcccccc tgacgacatg     1080
346 cctctctgga agccaatgat ctgtgctctg cagggtgggc cctctggccg tgatcatacg     1140
348 gtgctgactg gccccgcagg gccaaaggag ctctgggagc tgggtgtgga gcacagggct     1200
350 catgtgcttg tctctctttg cccacccaat gtcattgaga aggaattctg gccaacggag     1260
352 atgcagcccg tagtcacaga catggtgacg gtgcactggg tggctgagag cagcacagca     1320
354 ggctggttct gtacctctct cagggtcaca catggggaga gcaggaaagga aaggagggtg     1380
356 cagagactgc aatttccata cctggagcct gggcatgagc tgcccgcac caccctgctg     1440
358 ccttctctgg ctgctgtggg ccagtgtgtc tctcggggca acaacaagaa gccgggcaca     1500
360 ctgctcagcc actccaacaa ggggtgcaacc cagctgggca ccttctctgg catggagcag     1560
362 ctgctgcagc aggcagggtc tgagtgcacc gtggatatct ttaacgtggc cctgcagcag     1620
364 tctcaggcct gtggccttat gacccaacaa ctgaagcagt atgtctacct ctacaactgt     1680
366 ctgaacagcg cgttggcaga cgggctgccc
369 <210> SEQ ID NO: 10
370 <211> LENGTH: 570
371 <212> TYPE: PRT
372 <213> ORGANISM: HOMO SAPIENS
374 <220> FEATURE:
375 <221> NAME/KEY: Variant
376 <222> LOCATION: (46)..(46)
377 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.
380 <220> FEATURE:
381 <221> NAME/KEY: Variant
382 <222> LOCATION: (180)..(180)
383 <223> OTHER INFORMATION: wherein 'Xaa' is any amino acid.

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 162,200,203,214,224
Seq#:8; Xaa Pos. 49,110,121,127,142,155,166
Seq#:10; Xaa Pos. 46,180,201
Seq#:78; Xaa Pos. 2,3
Seq#:79; Xaa Pos. 5,6,7,8
Seq#:81; Xaa Pos. 2,3
Seq#:82; Xaa Pos. 5,6,7,8

VERIFICATION SUMMARY

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Input Set : A:\D0072.NP.msg.parts.ST25.txt

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L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:160
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:192
L:188 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:208
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:112
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:128
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:144
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:160
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:32
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:176
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:192
L:3182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:0
L:3216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
L:3248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
L:3282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0